

RAW SEQUENCE LISTING

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Application Serial Number: 10/554,408
Source: TFW0
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RAW SEQUENCE LISTING

DATE: 02/21/2007

PATENT APPLICATION: US/10/554,408

TIME: 14:05:30

Input Set : A:\2923-737.txt

Output Set: N:\CRF4\02212007\J554408.raw

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3 <110> APPLICANT: Grode, Leander
4   Kaufmann, Stefan H.E.
5   Raupach, Baerbel
6   Hess, Juergen
8 <120> TITLE OF INVENTION: Tuberculosis Vaccine with Improved Efficacy
10 <130> FILE REFERENCE: 2923-737
12 <140> CURRENT APPLICATION NUMBER: 10/554,408
13 <141> CURRENT FILING DATE: 2005-10-24
15 <150> PRIOR APPLICATION NUMBER: PCT/EP04/004345
16 <151> PRIOR FILING DATE: 2004-04-23
18 <150> PRIOR APPLICATION NUMBER: 60/464,644
19 <151> PRIOR FILING DATE: 2003-04-23
21 <160> NUMBER OF SEQ ID NOS: 2
23 <170> SOFTWARE: PatentIn version 3.3
25 <210> SEQ ID NO: 1
26 <211> LENGTH: 1881
27 <212> TYPE: DNA
28 <213> ORGANISM: Mycobacterium
31 <220> FEATURE:
32 <221> NAME/KEY: CDS
33 <222> LOCATION: (1)..(1878)
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37 Met Thr Asp Val Ser Arg Lys Ile Arg Ala Trp Gly Arg Arg Leu Met
38 1           5           10           15
40 atc ggc acg gca gcg gct gta gtc ctt ccg ggc ctg gtg ggg ctt gcc      96
41 Ile Gly Thr Ala Ala Ala Val Val Leu Pro Gly Leu Val Gly Leu Ala
42           20           25           30
44 ggc gga gcg gca acc gcg ggc gcg ttc tcc cgg ccg ggg ctg ccg gtc      144
45 Gly Gly Ala Ala Thr Ala Gly Ala Phe Ser Arg Pro Gly Leu Pro Val
46           35           40           45
48 gag tac ctg cag tct gca aag caa tcc gct gca aat aaa ttg cac tca      192
49 Glu Tyr Leu Gln Ser Ala Lys Gln Ser Ala Ala Asn Lys Leu His Ser
50 50          55          60
52 gca gga caa agc acg aaa gat gca tct gca ttc aat aaa gaa aat tca      240
53 Ala Gly Gln Ser Thr Lys Asp Ala Ser Ala Phe Asn Lys Glu Asn Ser
54 65          70          75          80
56 att tca tcc atg gca cca cca gca tct ccg cct gca agt cct aag acg      288
57 Ile Ser Ser Met Ala Pro Pro Ala Ser Pro Pro Ala Ser Pro Lys Thr
58          85          90          95
60 cca atc gaa aag aaa cac gcg gat gaa atc gat aag tat ata caa gga      336
61 Pro Ile Glu Lys Lys His Ala Asp Glu Ile Asp Lys Tyr Ile Gln Gly
62          100         105         110

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64	ttg gat tac aat aaa aac aat gta tta gta tac cac gga gat gca gtg	384
65	Leu Asp Tyr Asn Lys Asn Asn Val Leu Val Tyr His Gly Asp Ala Val	
66	115 120 125	
68	aca aat gtg ccg cca aga aaa ggt tac aaa gat gga aat gaa tat att	432
69	Thr Asn Val Pro Pro Arg Lys Gly Tyr Lys Asp Gly Asn Glu Tyr Ile	
70	130 135 140	
72	gtt gtg gag aaa aag aag aaa tcc atc aat caa aat aat gca gac att	480
73	Val Val Glu Lys Lys Lys Lys Ser Ile Asn Gln Asn Asn Ala Asp Ile	
74	145 150 155 160	
76	caa gtt gtg aat gca att tcg agc cta acc tat cca ggt gct ctc gta	528
77	Gln Val Val Asn Ala Ile Ser Ser Leu Thr Tyr Pro Gly Ala Leu Val	
78	165 170 175	
80	aaa gcg aat tcg gaa tta gta gaa aat caa cca gat gtt ctc cct gta	576
81	Lys Ala Asn Ser Glu Leu Val Glu Asn Gln Pro Asp Val Leu Pro Val	
82	180 185 190	
84	aaa cgt gat tca tta aca ctc agc att gat ttg cca ggt atg act aat	624
85	Lys Arg Asp Ser Leu Thr Leu Ser Ile Asp Leu Pro Gly Met Thr Asn	
86	195 200 205	
88	caa gac aat aaa atc gtt gta aaa aat gcc act aaa tca aac gtt aac	672
89	Gln Asp Asn Lys Ile Val Val Lys Asn Ala Thr Lys Ser Asn Val Asn	
90	210 215 220	
92	aac gca gta aat aca tta gtg gaa aga tgg aat gaa aaa tat gct caa	720
93	Asn Ala Val Asn Thr Leu Val Glu Arg Trp Asn Glu Lys Tyr Ala Gln	
94	225 230 235 240	
96	gct tat cca aat gta agt gca aaa att gat tat gat gac gaa atg gct	768
97	Ala Tyr Pro Asn Val Ser Ala Lys Ile Asp Tyr Asp Asp Glu Met Ala	
98	245 250 255	
100	tac agt gaa tca caa tta att gcg aaa ttt ggt aca gca ttt aaa gct	816
101	Tyr Ser Glu Ser Gln Leu Ile Ala Lys Phe Gly Thr Ala Phe Lys Ala	
102	260 265 270	
104	gta aat aat agc ttg aat gta aac ttc ggc gca atc agt gaa ggg aaa	864
105	Val Asn Asn Ser Leu Asn Val Asn Phe Gly Ala Ile Ser Glu Gly Lys	
106	275 280 285	
108	atg caa gaa gaa gtc att agt ttt aaa caa att tac tat aac gtg aat	912
109	Met Gln Glu Glu Val Ile Ser Phe Lys Gln Ile Tyr Tyr Asn Val Asn	
110	290 295 300	
112	gtt aat gaa cct aca aga cct tcc aga ttt ttc ggc aaa gct gtt act	960
113	Val Asn Glu Pro Thr Arg Pro Ser Arg Phe Phe Gly Lys Ala Val Thr	
114	305 310 315 320	
116	aaa gag cag ttg caa gcg ctt gga gtg aat gca gaa aat cct cct gca	1008
117	Lys Glu Gln Leu Gln Ala Leu Gly Val Asn Ala Glu Asn Pro Pro Ala	
118	325 330 335	
120	tat atc tca agt gtg gcg tat ggc cgt caa gtt tat ttg aaa tta tca	1056
121	Tyr Ile Ser Ser Val Ala Tyr Gly Arg Gln Val Tyr Leu Lys Leu Ser	
122	340 345 350	
124	act aat tcc cat agt act aaa gta aaa gct gct ttt gat gct gcc gta	1104
125	Thr Asn Ser His Ser Thr Lys Val Lys Ala Ala Phe Asp Ala Ala Val	
126	355 360 365	
128	agc gga aaa tct gtc tca ggt gat gta gaa cta aca aat atc atc aaa	1152

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129 Ser Gly Lys Ser Val Ser Gly Asp Val Glu Leu Thr Asn Ile Ile Lys
130      370      375      380
132 aat tct tcc ttc aaa gcc gta att tac gga ggt tcc gca aaa gat gaa      1200
133 Asn Ser Ser Phe Lys Ala Val Ile Tyr Gly Gly Ser Ala Lys Asp Glu
134 385      390      395      400
136 gtt caa atc atc gac ggc aac ctc gga gac tta cgc gat att ttg aaa      1248
137 Val Gln Ile Ile Asp Gly Asn Leu Gly Asp Leu Arg Asp Ile Leu Lys
138      405      410      415
140 aaa ggc gct act ttt aat cga gaa aca cca gga gtt ccc att gct tat      1296
141 Lys Gly Ala Thr Phe Asn Arg Glu Thr Pro Gly Val Pro Ile Ala Tyr
142      420      425      430
144 aca aca aac ttc cta aaa gac aat gaa tta gct gtt att aaa aac aac      1344
145 Thr Thr Asn Phe Leu Lys Asp Asn Glu Leu Ala Val Ile Lys Asn Asn
146      435      440      445
148 tca gaa tat att gaa aca act tca aaa gct tat aca gat gga aaa att      1392
149 Ser Glu Tyr Ile Glu Thr Thr Ser Lys Ala Tyr Thr Asp Gly Lys Ile
150      450      455      460
152 aac atc gat cac tct gga gga tac gtt gct caa ttc aac att tct tgg      1440
153 Asn Ile Asp His Ser Gly Gly Tyr Val Ala Gln Phe Asn Ile Ser Trp
154 465      470      475      480
156 gat gaa gta aat tat gat cct gaa ggt aac gaa att gtt caa cat aaa      1488
157 Asp Glu Val Asn Tyr Asp Pro Glu Gly Asn Glu Ile Val Gln His Lys
158      485      490      495
160 aac tgg agc gaa aac aat aaa agc aag cta gct cat ttc aca tcg tcc      1536
161 Asn Trp Ser Glu Asn Asn Lys Ser Lys Leu Ala His Phe Thr Ser Ser
162      500      505      510
164 atc tat ttg cca ggt aac gcg aga aat att aat gtt tac gct aaa gaa      1584
165 Ile Tyr Leu Pro Gly Asn Ala Arg Asn Ile Asn Val Tyr Ala Lys Glu
166      515      520      525
168 tgc act ggt tta gct tgg gaa tgg tgg aga acg gta att gat gac cgg      1632
169 Cys Thr Gly Leu Ala Trp Glu Trp Trp Arg Thr Val Ile Asp Asp Arg
170      530      535      540
172 aac tta cca ctt gtg aaa aat aga aat atc tcc atc tgg ggc acc acg      1680
173 Asn Leu Pro Leu Val Lys Asn Arg Asn Ile Ser Ile Trp Gly Thr Thr
174 545      550      555      560
176 ctt tat ccg aaa tat agt aat aaa gta gat aat cca atc gaa tat gca      1728
177 Leu Tyr Pro Lys Tyr Ser Asn Lys Val Asp Asn Pro Ile Glu Tyr Ala
178      565      570      575
180 tta gcc tat gga agt cag ggt gat ctt aat cca tta att aat gaa atc      1776
181 Leu Ala Tyr Gly Ser Gln Gly Asp Leu Asn Pro Leu Ile Asn Glu Ile
182      580      585      590
184 agc aaa atc att tca gct gca gtt ctt tcc tct tta aca tcg aag cta      1824
185 Ser Lys Ile Ile Ser Ala Ala Val Leu Ser Ser Leu Thr Ser Lys Leu
186      595      600      605
188 cct gca gag ttc gtt agg cgc gga tcc gga att cga agc tta tcg atg      1872
189 Pro Ala Glu Phe Val Arg Arg Gly Ser Gly Ile Arg Ser Leu Ser Met
190      610      615      620
192 tcg acg tag      1881
193 Ser Thr

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194 625
197 <210> SEQ ID NO: 2
198 <211> LENGTH: 626
199 <212> TYPE: PRT
200 <213> ORGANISM: Mycobacterium
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212 Gly Gly Ala Ala Thr Ala Gly Ala Phe Ser Arg Pro Gly Leu Pro Val
213 35 40 45
216 Glu Tyr Leu Gln Ser Ala Lys Gln Ser Ala Ala Asn Lys Leu His Ser
217 50 55 60
220 Ala Gly Gln Ser Thr Lys Asp Ala Ser Ala Phe Asn Lys Glu Asn Ser
221 65 70 75 80
224 Ile Ser Ser Met Ala Pro Pro Ala Ser Pro Pro Ala Ser Pro Lys Thr
225 85 90 95
228 Pro Ile Glu Lys Lys His Ala Asp Glu Ile Asp Lys Tyr Ile Gln Gly
229 100 105 110
232 Leu Asp Tyr Asn Lys Asn Asn Val Leu Val Tyr His Gly Asp Ala Val
233 115 120 125
236 Thr Asn Val Pro Pro Arg Lys Gly Tyr Lys Asp Gly Asn Glu Tyr Ile
237 130 135 140
240 Val Val Glu Lys Lys Lys Lys Ser Ile Asn Gln Asn Asn Ala Asp Ile
241 145 150 155 160
244 Gln Val Val Asn Ala Ile Ser Ser Leu Thr Tyr Pro Gly Ala Leu Val
245 165 170 175
248 Lys Ala Asn Ser Glu Leu Val Glu Asn Gln Pro Asp Val Leu Pro Val
249 180 185 190
252 Lys Arg Asp Ser Leu Thr Leu Ser Ile Asp Leu Pro Gly Met Thr Asn
253 195 200 205
256 Gln Asp Asn Lys Ile Val Val Lys Asn Ala Thr Lys Ser Asn Val Asn
257 210 215 220
260 Asn Ala Val Asn Thr Leu Val Glu Arg Trp Asn Glu Lys Tyr Ala Gln
261 225 230 235 240
264 Ala Tyr Pro Asn Val Ser Ala Lys Ile Asp Tyr Asp Asp Glu Met Ala
265 245 250 255
268 Tyr Ser Glu Ser Gln Leu Ile Ala Lys Phe Gly Thr Ala Phe Lys Ala
269 260 265 270
272 Val Asn Asn Ser Leu Asn Val Asn Phe Gly Ala Ile Ser Glu Gly Lys
273 275 280 285
276 Met Gln Glu Glu Val Ile Ser Phe Lys Gln Ile Tyr Tyr Asn Val Asn
277 290 295 300
280 Val Asn Glu Pro Thr Arg Pro Ser Arg Phe Phe Gly Lys Ala Val Thr
281 305 310 315 320
284 Lys Glu Gln Leu Gln Ala Leu Gly Val Asn Ala Glu Asn Pro Pro Ala
285 325 330 335
288 Tyr Ile Ser Ser Val Ala Tyr Gly Arg Gln Val Tyr Leu Lys Leu Ser

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289          340          345          350
292 Thr Asn Ser His Ser Thr Lys Val Lys Ala Ala Phe Asp Ala Ala Val
293          355          360          365
296 Ser Gly Lys Ser Val Ser Gly Asp Val Glu Leu Thr Asn Ile Ile Lys
297          370          375          380
300 Asn Ser Ser Phe Lys Ala Val Ile Tyr Gly Gly Ser Ala Lys Asp Glu
301 385          390          395          400
304 Val Gln Ile Ile Asp Gly Asn Leu Gly Asp Leu Arg Asp Ile Leu Lys
305          405          410          415
308 Lys Gly Ala Thr Phe Asn Arg Glu Thr Pro Gly Val Pro Ile Ala Tyr
309          420          425          430
312 Thr Thr Asn Phe Leu Lys Asp Asn Glu Leu Ala Val Ile Lys Asn Asn
313          435          440          445
316 Ser Glu Tyr Ile Glu Thr Thr Ser Lys Ala Tyr Thr Asp Gly Lys Ile
317          450          455          460
320 Asn Ile Asp His Ser Gly Gly Tyr Val Ala Gln Phe Asn Ile Ser Trp
321 465          470          475          480
324 Asp Glu Val Asn Tyr Asp Pro Glu Gly Asn Glu Ile Val Gln His Lys
325          485          490          495
328 Asn Trp Ser Glu Asn Asn Lys Ser Lys Leu Ala His Phe Thr Ser Ser
329          500          505          510
332 Ile Tyr Leu Pro Gly Asn Ala Arg Asn Ile Asn Val Tyr Ala Lys Glu
333          515          520          525
336 Cys Thr Gly Leu Ala Trp Glu Trp Trp Arg Thr Val Ile Asp Asp Arg
337          530          535          540
340 Asn Leu Pro Leu Val Lys Asn Arg Asn Ile Ser Ile Trp Gly Thr Thr
341 545          550          555          560
344 Leu Tyr Pro Lys Tyr Ser Asn Lys Val Asp Asn Pro Ile Glu Tyr Ala
345          565          570          575
348 Leu Ala Tyr Gly Ser Gln Gly Asp Leu Asn Pro Leu Ile Asn Glu Ile
349          580          585          590
352 Ser Lys Ile Ile Ser Ala Ala Val Leu Ser Ser Leu Thr Ser Lys Leu
353          595          600          605
356 Pro Ala Glu Phe Val Arg Arg Gly Ser Gly Ile Arg Ser Leu Ser Met
357          610          615          620
360 Ser Thr
361 625

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VERIFICATION SUMMARY

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Input Set : A:\2923-737.txt

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